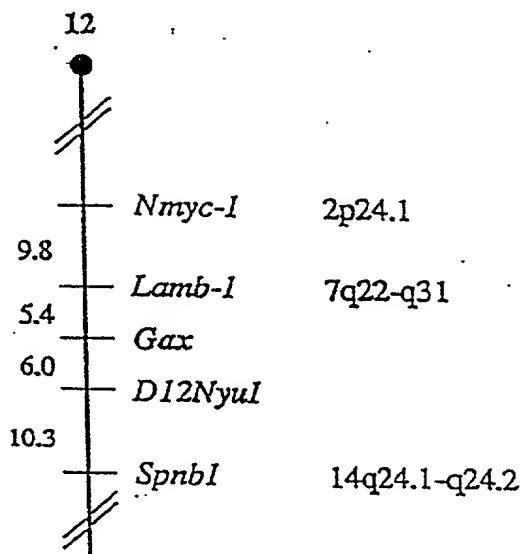
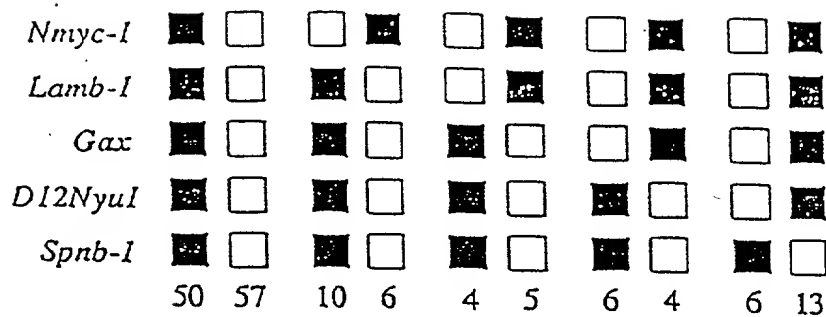


Figure 1

CTCAAGTCTTTATACGTGCAGGAGACTGGCCGCTCGGCTCAGGACTGGGATTAGCGGGCTCTGCTCAAAACCCGCGCGCTTTTACATTAGGAGTGAGTGG 100
 GGGAGAGTCTAGGATTCTAGTGAAAAGTGACAGCGCTTGGTGGACTTTGGGACCTTCGTGAAGTCTTCTGCTTGGAAAGCTGAGACTTGCATGCC ATG 199
 E H P L F G C L R S P H A T A Q G L H P F S Q S S 1
 GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT 274
 L A L H G R S D H H S Y P E L S T S S S S C I I A 26
 CTG GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA TCT TCC TCG TCT TGC ATA ATC GCG 349
 L A L H G R S D H H S Y P E L S T S S S S C I I A 51
 GGA TAC CCC AAT GAG GAG GGC ATG TTT GCC AGC CAG CAT CAC AGC GCG CAC CAC CAC CAC CAC CAC CAC CAC CAT 424
 G Y P N E E G H F A S Q H H R G H H H H H H H H H H 76
 CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC 499
 H H H Q Q Q Q Q H Q A L Q S N W H L P Q M S S P P S 101
 GCG GCC CGG CAC AGC CTT TGC CTG CAG CCT GAT TCC GGA GGG CCC CCG GAG CTG GGG AGC AGC CCT CCG GTC CTG 574
 A A R H S L C L Q P D S G G P P E L G S S P P V L 126
 TGC TCC AAC TCT TCT AGC CTG GGC TCC AGC ACC CCG ACC GGA GCC GCG TGC GCA CCA AGG GAT TAT GGC CGT CAA 649
 C S N S S S L G S S T P T G A A C A P R D Y G R Q 151
 GCG CTG TCA CCC GCA GAA GTG GAG AAG AGA AGT GGC AGC AAA AGA AAA AGC GAC AGT TCA GAT TCC CAG GAA GGA 724
 A L S P A E V E K R S G S K R K S D S S D S Q E G 176
 AAT TAC AAG TCA GAA GTG AAC AGC AAA CCT AGG AAG GAA AGA ACA GCT TTC ACC AAA GAG CAA ATC AGA GAA CTT 799
 N Y K S E V N S K P R K Z R T A F T K Z Q I R E L 201
 GAG GCA GAG TTC GCC CAT CAT AAC TAT CTG ACC AGA CTG AGA AGA TAT GAG ATA GCG GTG AAC CTA GAC CTC ACT 874
 E A E F A H H N Y L T R L R R Y E I A V N L D L T 226
 GAA AGA CAG GTG AAA GTG TGG TTC CAG AAC AGG AGA ATG AAG TGG AAG CCG GTC AAG GGG GGA CAA CAA GGA GCT 949
 E R Q V K V N F Q N R R H K N K R V K G G Q Q G A 251
 GCA GCC CGA GAA AAG GAA CTG GTG AAT GTG AAA AAG GGA ACA CTT CTT CCA TCA GAG CTG TCA GGA ATT GGT GCA 1024
 A A R E K E L V N V K K G T L L P S E L S G I G A 276
 GCC ACC CTC CAG CAG ACA GGG GAC TCA CTA GCA AAT GAC GAC AGT CCG GAT AGT GAC CAC AGC TCT GAG CAC GCA 1099
 A T L Q Q T G D S L A N D D S R D S D H S S E H A 301
 CAC TTA TGA TACATACAGAGACCAGCTCCGTTCTCAGGAAGCACCATTGTGATGGCAATCTCACCCAAACATCGTTTACATGGCAGATGACTGTG 1196
 H L stop 303
 GCAGTGTGCTTAATATAATTAAACGAGGATCTCAAGTCTGTTTCTCATGATGATAGAAGGTTTACACTAAGTGCCTCTTATTGAAGATGCTTCEAC 1296
 AGTGAATTTGGAGAAAGTGAACATATCTAAATATCTTGTTCCTTATATGACAGAGAGGAGATGAATGTTTGGCTTTGGCTTGCACTGAAATTTAAATTG 1396
 CTACCAAGAGCAAACTCGGTAAGACATTTTGACTCAAGTTGTCTCCAGAGTGAAGATGTTATAGAATGCTTTGAACATTCCAGTTGTACCAGGTCAATG 1496
 GTGTGACACTGGGCAGGTATTTGCTTTTGTCTGCACTGAAACTTAACTGCTATCAAGTTAACCCATGAATAGTTTATCTTGAACAGCCACAGTGCCTG 1596
 AAATCACCAGTGGATATAAAATGAAGTGAATTCGTATATATTACTCTTAAGTCAATTTTCTGTCTTCACTAATTTTAGCAAAATGCATTATATTAGC 1696
 TGATGAAAATAGGCTTTCCCGTGCACAAATGCAGCCAGCTTCTGTATTTTATACATTTTGTCTGCTCAGACACATCAGTATGTGCTTACTTGTGTT 1796
 CAAGTAGAGGAAATGCAGTAGAGTCTGATAGGACATATTCTTGGTACCACAGACAAAACAAATCTTCTGTTCATGACTATCAACTGCTGCAGATACAT 1896
 TAGAGAACACACCTAGCCCCCTCCAGCCTCCCTCTGTTATCTGCTCGAAGACATTAGCGTCATAGGCAAGTAGTTACCTTGCCAAATGAGTCTTGTGTGG 1996
 CAGATGCTGTATTTGTATCTTTAAACTGTTAATGGTATGTCTGCTTCAGTTAACAGGGAAAAAGATTTCTTCTCATTTGTTATGATACAAAACCA 2096
 AGTGCCAAACAAAGCTAGTTCTTCAAGGGATAGATGAGAACTGAATGTCTGACAAGTAGACTCAGCGAAAATACATTTATTTTTCAGAGGCTGTGTATTC 2196
 ATGCAGTACAAGTCTTGTATTTGTAAAAAAAAGTTAAATATG 2244

Figure 2



102220 22904660

[illegible]

Figure 3

Figure 4

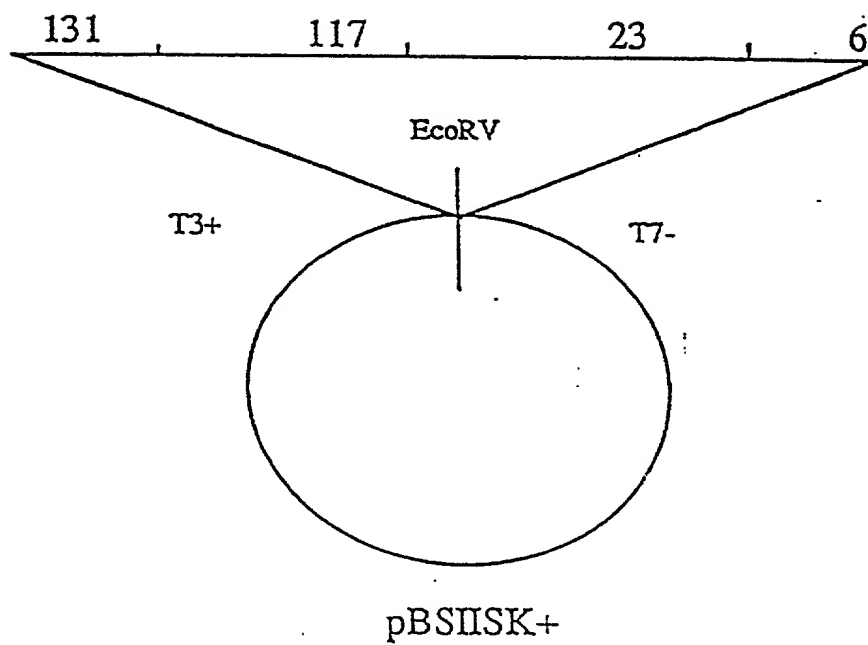
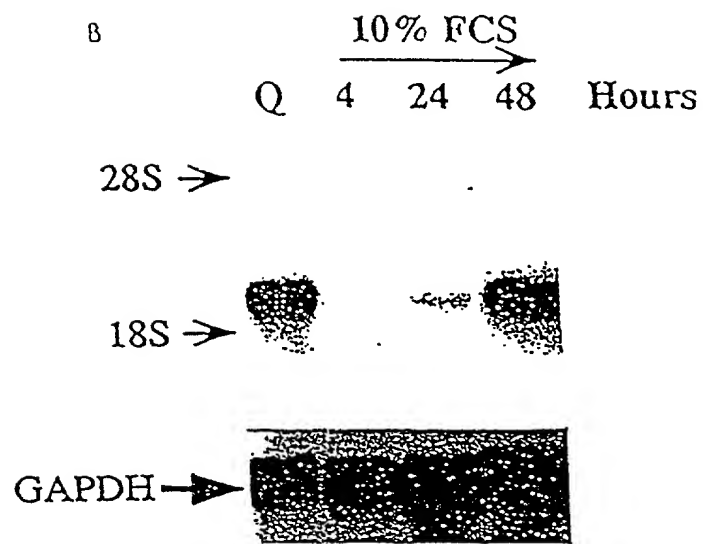


Figure 5a



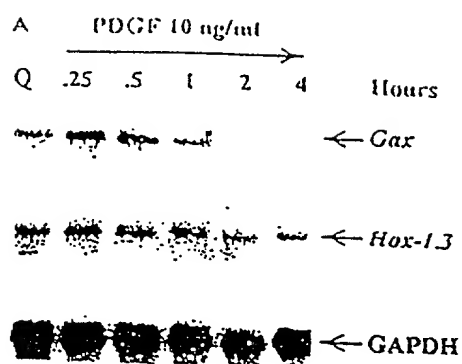
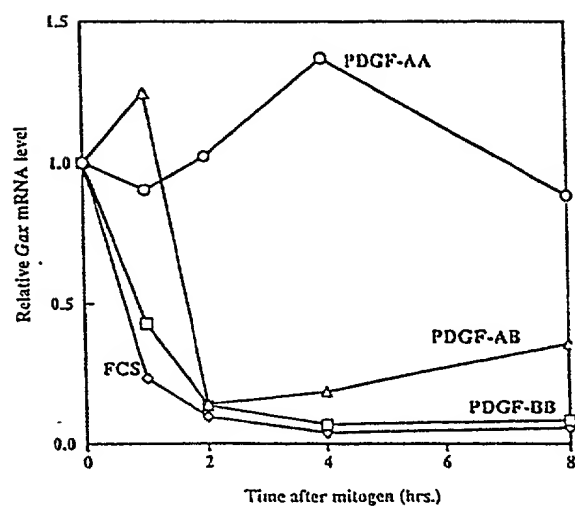


Figure 6



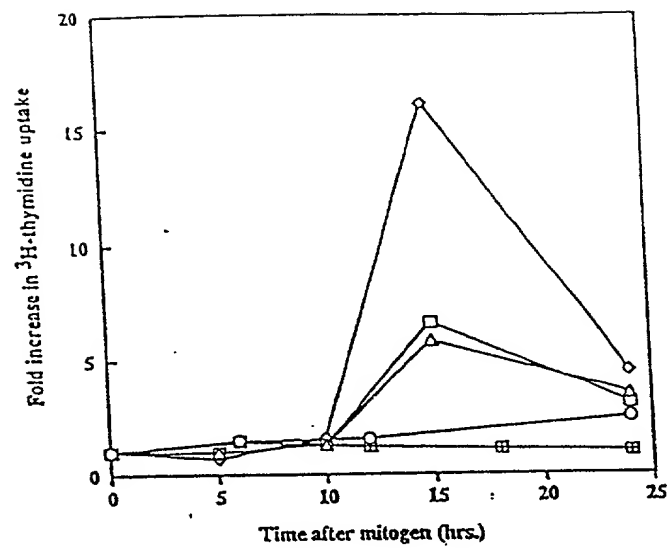


Figure 7

Figure 8

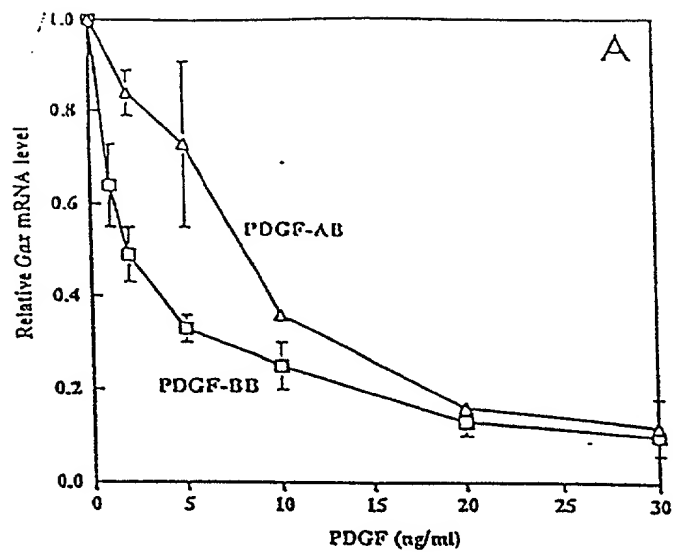


Figure 9

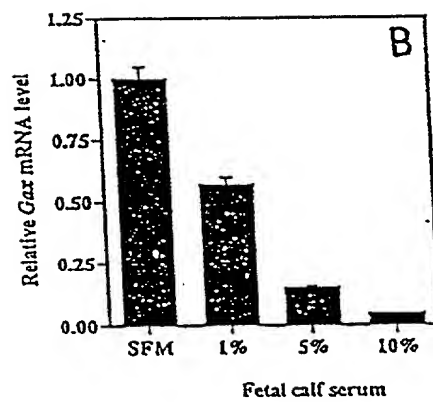
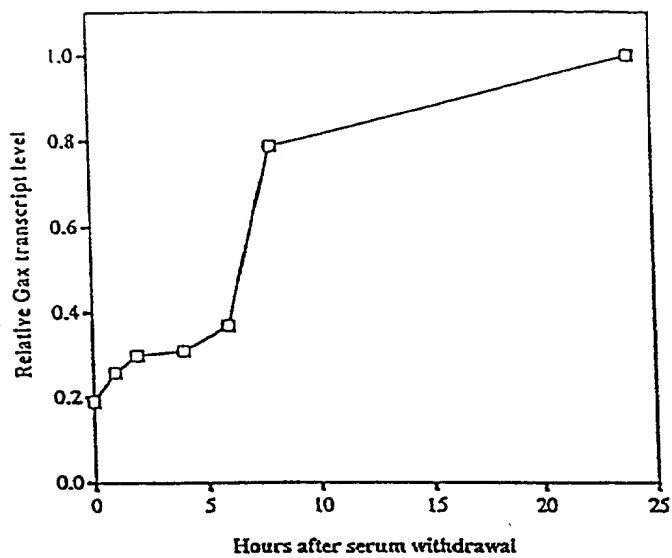


Figure 10



FOI 2008-004650

Figure 11

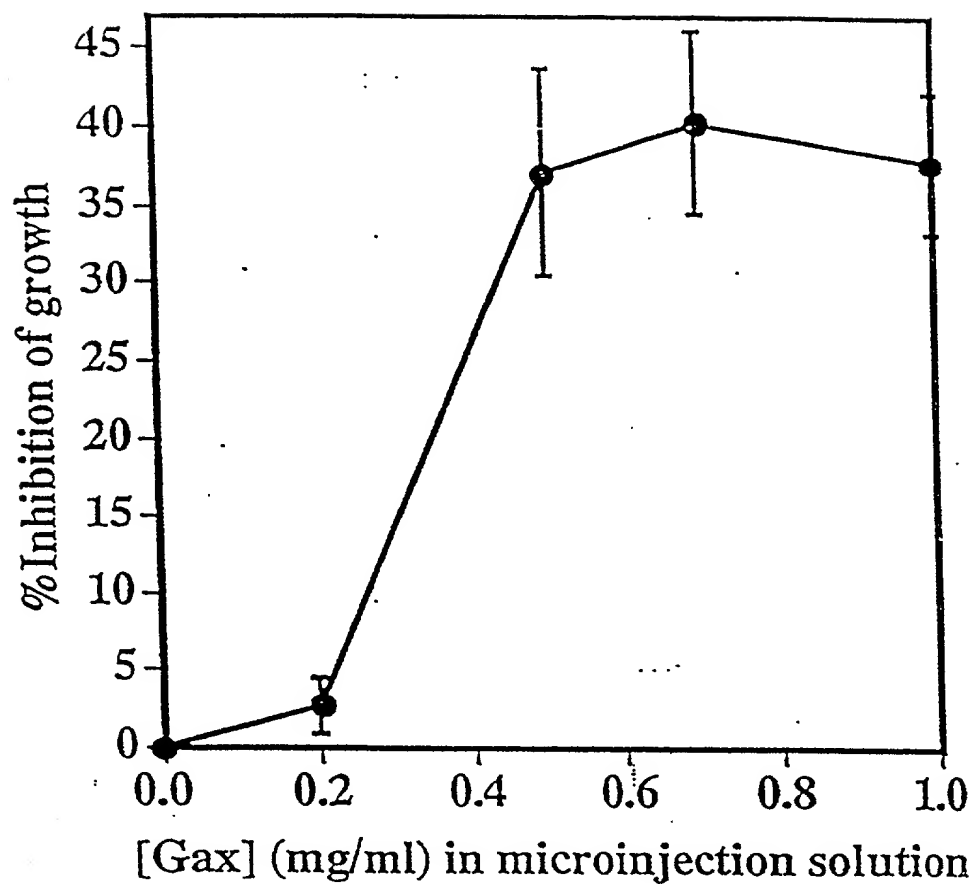


Figure 10

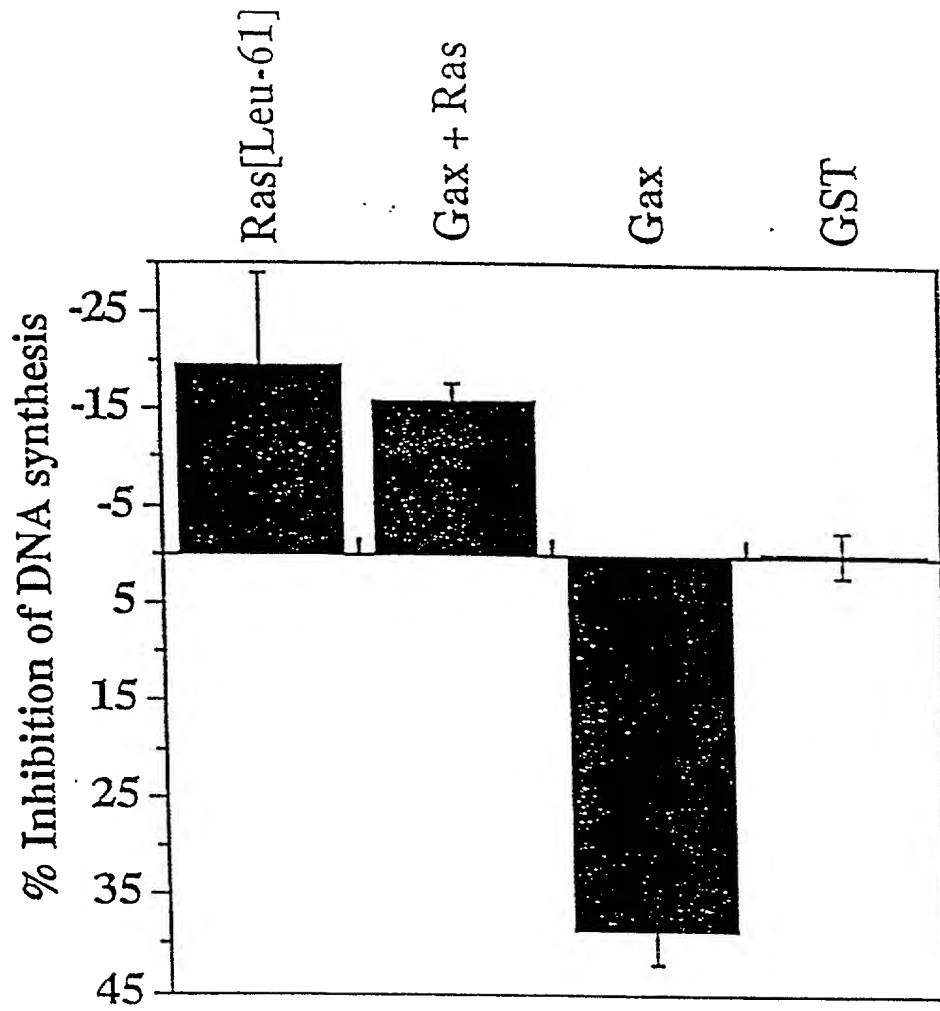
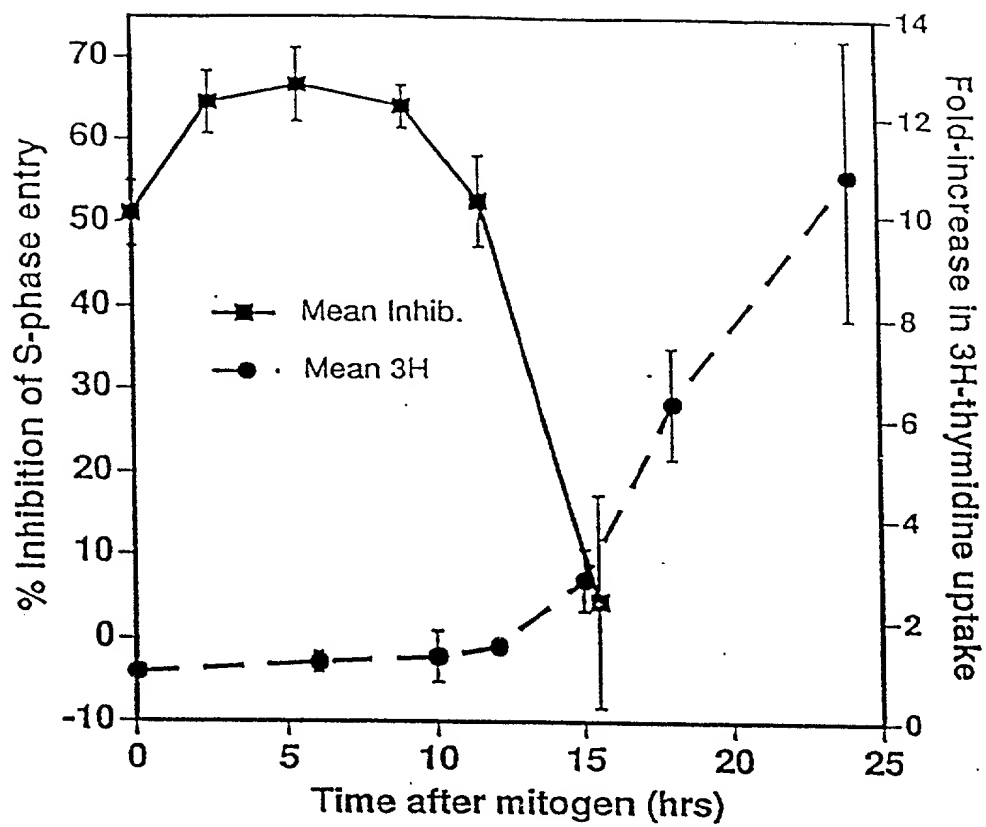
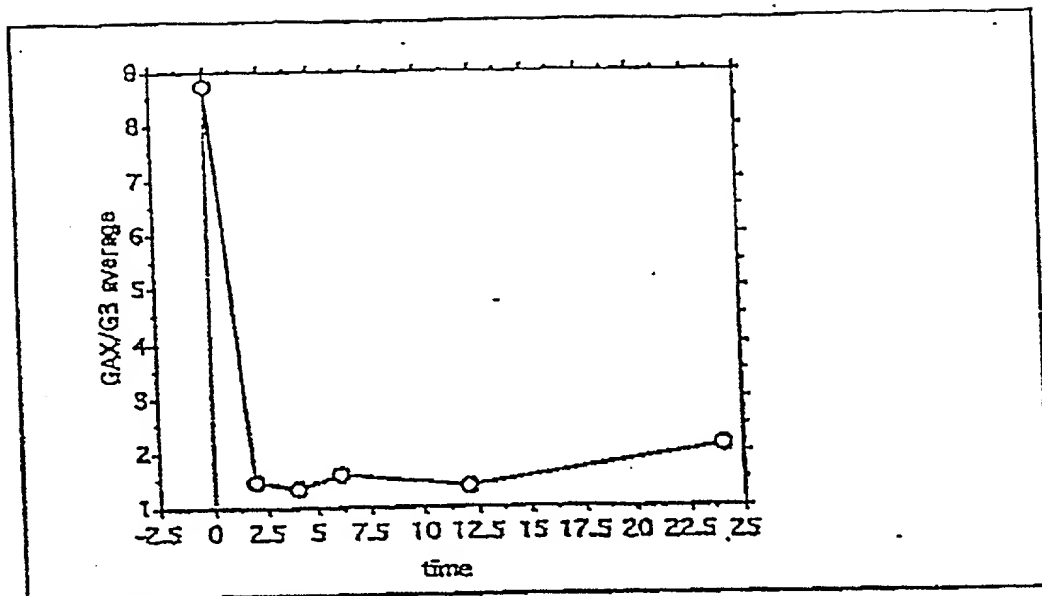


Figure 13B



05940673.082701
FD 280 E 904680

Figure 14



10/20/2020 10:20:20